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(54) Title: NUCLEIC ACID ARCHIVING

(57) Abstract

This invention is directed to a process for irreversibly binding nucleic acid to solid phase and corresponding processes for the utilization thereof. Nucleic acid is bound to solid phase matrixes exhibiting sufficient hydrophilicity and electropositivity to irreversibly bind the nucleic acids from a sample. These processes include nucleic acid (double or single stranded DNA and RNA) capture from high volume: low concentration specimens, buffer changes, washes, and volume reductions, and enable the interface of solid phase bound nucleic acid with enzyme, hybridization or amplification strategies. The invention, solid phase irreversibly bound nucleic acid, may be used, for example, in repeated analyses to confirm results or test additional genes in both research and commercial applications. Further, a method is described for virus extraction, purification, and solid phase amplification from large volume plasma specimens.

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NUCLEIC ACID ARCHIVING

FIELD OF INVENTION

This invention relates to the general fields of molecular biology, biochemistry, genetics, and biological research, and specifically, relates to a method for capturing and irreversibly binding nucleic acid from any biological specimen onto a solid phase matrix such that the bound nucleic acid can be washed extensively with aqueous buffers without elution from the solid phase. Further, the solid phase bound nucleic acid can be utilized directly as an accessible substrate for enzyme reactions or hybridization primer or probe complementary base pairing and subsequent detection, either with or without amplification. Solid phase bound nucleic acid can be introduced into hybridization or amplification reactions, not just once, but multiple times. This method, thus, further relates to commercial applications interfacing nucleic acid capture with nucleic acid hybridization and/or amplification.

BACKGROUND AND PRIOR ART

The molecular structure of nucleic acids provides for specific detection by means of complementary base pairing of oligonucleotide probes or primers to sequences that are unique to specific target organisms or tissues. Since all biological organisms or specimens contain nucleic acid of specific and defined sequences, a universal strategy for nucleic acid detection has extremely broad application in a number of diverse research and development areas as well as commercial industries. The potential for practical uses of nucleic acid detection was greatly enhanced by the description of methods to amplify or copy, with fidelity, precise sequences of nucleic acid found at low concentration to much higher copy numbers, so that they are more readily observed by detection methods.

The original amplification method is the polymerase chain reaction described by Mullis *et al.* (United States Patent No. 4,683,195, United States Patent No. 4,683,202, and United States Patent 4,965,188, all specifically incorporated herein by reference). Subsequent to the introduction of PCR, a wide array of strategies for amplification have been described. See, for

example, United States Patent No. 5,130,238 to Malek, nucleic acid sequence based amplification (NASBA); United States Patent No. 5,354,668 to Auerbach, isothermal methodology; United States Patent No. 5,427,930 to Buirkenmeyer, ligase chain reaction; and, United States Patent No. 5,455,166 to Walker, strand displacement amplification (SDA); all specifically incorporated herein by reference. Some of these amplification strategies, such as SDA or NASBA, require a single stranded nucleic acid target. The target is commonly rendered single stranded via a melting procedure using high temperature prior to amplification. The instant invention provides a novel mechanism for converting double stranded nucleic acid to single stranded nucleic acid without that conventional melting step.

Prior to nucleic acid amplification and detection, the target nucleic acid must be extracted and purified from the biological specimen such that inhibitors of amplification reaction enzymes are removed. Further, a nucleic acid target that is freely and consistently available for primer annealing must be provided. A wide variety of strategies for nucleic acid purification are known. These include, for example, phenol-chloroform and/or ethanol precipitation (Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.), high salt precipitation (Dykes (1988) *Electrophoresis* **9**:359-368), proteinase K digestion (Grimberg *et al.* (1989) *Nucleic Acids Res* **22**:8390), chelex and other boiling methods (Walsh *et al.* (1991) *Bio/techniques* **10**:506-513) and solid phase binding and elution (Vogelstein and Gillespie (1979) *Proc. Nat. Acad. Sci. USA* **76**:615-619, all of which are specifically incorporated herein by reference).

The analysis of nucleic acid targets therefore consists of three steps: nucleic acid extraction/purification from biological specimens, direct probe hybridization or amplification of the specific target sequence, and specific detection thereof. In currently employed conventional protocols each of these three steps is performed separately, making nucleic acid analysis labor intensive. Further, numerous manipulations, instruments and reagents are necessary to perform each step of the analysis.

Another concern with current methodologies is the significant chance of

specimen cross contamination; between concurrently run specimens or a from previously amplified sample. It would be advantageous to eliminate the melt step necessary for generating single strand nucleic acid for probe hybridization or amplification primer annealing, and directly integrate the three nucleic acid analysis steps so as to simplify the analysis procedure and methodologies, as well as reduce and/or remove the risk of cross contamination. The invention discussed herein provides a method for a direct interface of the extraction and hybridization or amplification steps discussed above.

For analysis purposes, nucleic acid must frequently be extracted from extremely small specimens in which it is difficult, if not impossible, to obtain a second confirmatory specimen. Examples include analysis of crime scene evidence or fine needle biopsies for clinical testing. In such examples, the extent of the genetic testing and confirmation through replica testing is, thus, limited by the nucleic acid specimen size. Using conventional extraction protocols for these small specimens, the nucleic acid is often lost or yields are such that only a single or few amplification analyses are possible. The present invention provides a method for irreversibly binding and thus, permanently archiving, nucleic acid from specimens. That is to say, the nucleic acid is neither altered nor exhausted during analysis, and therefore, is able to be reanalyzed an unlimited number of times. This invention takes advantage of solid phase DNA binding properties known but believed by the skilled artisan to be incompatible with nucleic acid analysis. In addition, binding properties of use for RNA analysis are characterized.

Specimens that contain high levels of endogenous or background nucleic acid such as blood are extremely difficult to analyze for the presence of low level specific targets. Solid phases with high nucleic acid avidity can be utilized to irreversibly capture oligonucleotide or probe sequences. By changing buffer conditions these materials can then selectively capture target sequences even in the presence of high levels of background nucleic acid.

The requirements for binding of DNA to solid phases and subsequently being able to elute them therefrom have been described by Boom (United States Patent No. 5,234,809, specifically incorporated herein by reference) and

Woodard (United States Patent No. 5,405,951, United States Patent No. 5,438,129, United States Patent No. 5,438,127, all specifically incorporated herein by reference). Specifically, DNA binds to solid phases that are electropositive and hydrophilic. Solid phase materials consisting of the atoms Silicon (Si), Boron (B), or Aluminum (Al) can be rendered sufficiently hydrophilic by hydroxyl (-OH) or other groups to result in a surface that irreversibly binds DNA, while proteins or inhibitors do not bind. The binding of RNA has not been previously characterized and is revealed in the present invention. Since conventional purification methods require elution of the bound nucleic acid, these solid phase materials are described as being of no use for DNA purification. In fact, considerable effort has been expended to derive solid phase materials sufficiently electropositive and hydrophilic to adequately bind nucleic acid and yet allow for its elution therefrom. (See, for example, United States Patent Nos. 5,523,392, 5,525,319 and 5,503,816 all to Woodard, all specifically incorporated herein by reference). The present invention uses solid phase matrixes to irreversibly bind nucleic acid and teaches methods for direct solid phase nucleic acid manipulation, hybridization, and/or amplification. That is, analysis is performed without elution of the nucleic acid from the solid phase.

Boom, *supra,* describes solid phase DNA amplification using high chaotropic salt to reversibly bind to silica. When this solid phase is placed in the amplification reaction buffer, the nucleic acid is, in fact, eluted. Therefore, the amplification actually occurs in solution not on solid phase. Furthermore, since binding is not irreversible, the amplification can only be performed once. Del Rio *et al.* ((1996) *Bio/techniques* **20**:970-974) describe filter entrapment of nucleic acid in a manner allowing for repeat amplification. However, they do not describe a binding mechanism that is irreversible, therefore the method is only recommended for analysis of higher nucleic acid concentrations and then, only for a limited number of analyses.

The instant invention is directed to a novel method for converting double stranded nucleic acid to single stranded nucleic acid without any melting step and provides methods for rapid DNA and RNA capture that directly

interfaces extraction and purification with either hybridization or amplification. The present invention further provides a method for irreversibly binding, and thus, permanently archiving nucleic acid from specimens. The present invention uses solid phase matrixes to irreversibly bind nucleic acid and teaches true, direct solid phase manipulation and analyses including enzyme recognition, hybridization, and primer dependent amplification. True solid phase analysis provides for stringent aqueous washes, rapid automatable nucleic acid capture and purification, selective nucleic acid detection, repeat and/or expanded analysis of the bound nucleic acid, and long term storage of nucleic acid. Each of these disclosed methodologies overcomes the drawbacks of the prior art.

SUMMARY OF THE INVENTION

The instant invention is based on novel methods of using solid phases to irreversibly capture RNA, DNA or other nucleic acids as a means for: aqueous washes, buffer changes and volume reductions during procedural manipulations; rapid and immediate capture of nucleic acid as a method of automating extraction; integrating nucleic acid capture and purification with oligonucleotide or probe hybridization or target or signal amplification for direct analysis of nucleic acid bound to the solid phase as either single or double strands; repeat and/or expanded analysis of the bound nucleic acid following its capture onto the solid phase matrix (nucleic acid archiving); and, gravity or high flow rate solid phase chromatography as a means of either concentrating nucleic acid from large volume specimens or removing contaminant nucleic acid from aqueous buffers or solutions.

More specifically, this invention comprises the use of highly electropositive solid phase materials, generally containing Si, B, or Al atoms rendered hydrophilic by -OH or other groups, so as to result in a surface that irreversibly captures nucleic acid. Using these high affinity materials, nucleic acid is captured as double stranded nucleic acid directly from aqueous biological specimens or buffers. By adjustment of the specimen to alkaline pH or high chaotropic salt concentration, the nucleic acid is bound to the solid phase as single strand nucleic acid. Binding the nucleic acid as a single strand

is necessary in order to interface with hybridization or isothermal amplification methods. The solid phase bound nucleic acid can be readily washed with aqueous buffers, thereby providing a convenient mechanism for buffer changes and volume reduction. In the preferred embodiment, this is accomplished utilizing gravity flow. The solid phase bound nucleic acid can be directly brought into contact with reaction mixtures that provide for nucleic acid hybridization, signal or target amplification. The nucleic acid remains bound to the solid phase even after multiple buffer washes, hybridization, or amplification reactions. The ability to reanalyze the same nucleic acid specimen is a mechanism that provides a means of result confirmation and/or expanded analysis, especially useful when the specimen is available in limited quantity or cannot be replaced. Irreversibly bound nucleic acid is stable at ambient room temperature, further providing a useful method of nucleic acid storage.

The invention described herein provides a method for capturing and irreversibly binding nucleic acid, at low concentrations and at high flow rates from any biological specimen onto a solid phase matrix, such that the bound nucleic acid can be washed extensively with aqueous buffers without elution from the solid phase. This binding provides high stringency for commercial applications such as microarray hybridizations that demand low background to attain high sensitivity. This method, thus, further relates to commercial applications for automating nucleic acid extraction, concentrating low copy nucleic acid from high volume specimens, and interfacing extraction and purification with amplification or hybridization nucleic acid capture. Commercial applications include high throughput nucleic acid testing that would benefit from robotic automation, or economical screening of low prevalence targets by means of pooled specimen testing. Further, the solid phase bound nucleic acid can be directly manipulated by enzyme, hybridization, or amplification reactions, not just once, but multiple times. The present invention therefore further lends itself to applications where a biological specimen is found in limited quantity and/or might be irreplaceable and the reanalysis either immediately or after storage of the original specimen is beneficial. Areas where this occurs include, for example, forensics, medical and biological

research, veterinary or human clinical diagnostics, dentistry, environmental, food, or water microbiology, and agricultural or other industrial applications.

Other features and advantages of the instant invention will become apparent from the following detailed description, taken in conjunction with the accompanying figures, that illustrate by way of example, the principles of the instant invention.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a bar graph illustrating the percentage binding of 1 nanogram of ^{32}P radiolabeled DNA to 198 mg of either aluminum oxide or aluminum hydroxide following one hour room temperature incubation with rotation in water, 0.1 N Sodium Hydroxide (NaOH), or 4 M guanidine thiocyanate (GuSCN) binding buffers.

Figure 2 shows the effect of increasing DNA concentration on the binding efficiency of ^{32}P radiolabeled DNA to 198 mg aluminum oxide following one hour room temperature incubation with rotation in water, 0.1 N NaOH, or 4 M guanidine thiocyanate binding buffers.

Figure 3 demonstrates that DNA bound to aluminum oxide is irreversibly bound with greater than 90% retained even after 10 washes with either 70% ETOH, water, or PCR buffer at 95 C.

Figure 4 compares the effect of flow rate and concentration on DNA binding to silica dioxide versus aluminum oxide.

Figures 5a and 5b illustrate simultaneous binding of 106 copies of HIV DNA and 1µl of a plasmid prep of mycobacterium DNAs to aluminum oxide in water followed by direct solid phase amplification of the two targets in series. HIV was initially amplified using 35 cycles of polymerase chain reaction (PCR), followed by amplification of the mycobacterium target using strand

agarose gel of HIV amplification product. Well 1 is a molecular weight ladder, wells 2,3 are positive aqueous 1000 copy control amplifications, wells 4,5,6, and 7 are aluminum solid phase PCR amplifications, wells 8,9,10, and 11 are negative aluminum solid phase controls, wells 12,13 are aqueous negative controls. Figure 5b depicts an ethidium bromide stained agarose gel of the SDA amplification products. Wells 1,2 are aqueous positive controls, wells 3,4,5, and 6 are aluminum solid phase SDA amplifications, wells 7,8,9, and 10 are negative aluminum controls, and 11, 12 are aqueous negative controls.

Figure 6 shows excellent amplification of aluminum bound RNA following ethidium staining of an agarose gel of the rtTH PCR product produced from HIV RNA guanidine extracted from 0.5 ml plasma of an AIDS patient. Well 1 = molecular weight ladder, well 2 = 1000 copy positive aqueous control HIV DNA, wells 3,4, and 5 = rtTH PCR product following three separate guanidine aluminum oxide extractions, well 6,7 = aluminum oxide negative controls, well 8 = aqueous negative control.

Figure 7 depicts the silver stained pattern for the Promega STR CTT multiplex which was the fourth gene set amplified, and the Promega FFV multiplex which was the fifth gene set amplified. Lane 1,8,9,16 are allelic ladders, lane 17 is human genomic aqueous positive control, lanes 2,3,4 are fourth amplification (CTT multiplex) on aluminum oxide bound DNA, lanes 5,6,7 and aluminum CTT negative controls, lanes 10,11,12 are the fifth aluminum oxide FFV multiplex amplification products, lanes 13,14, 15 are the aluminum FFV negative controls.

Figure 8 depicts percent radiolabeled DNA bound to either aluminum oxide or silica dioxide for various starting volumes and at different flow rates.

Figure 9 depicts solid phase PCR amplification as confirmed by EtBr agarose gel using HLA DRbcta primers following irreversible capture for different capture times after addition of 50 µl ACD anticoagulated blood in the

presence of 0.1 N NaOH and aluminum oxide.

Figure 10 is a PCR amplification tube incorporating solid phase binding material for automated nucleic acid extraction.

Figure 11 illustrates limit of PCR amplification detection for a pure RNA target (pAW 109) following either direct binding onto aluminum oxide or following hybridization to an aluminum oxide irreversibly bound oligonucleotide capture probe.

Figure 12 shows low copy detection of HIV spiked into 5.5 ml plasma following guanidium extraction and hybridization capture to aluminum oxide HIV capture beads at a final hybridization reaction volume of 28 ml.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

It is understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention as claimed.

The general principles and conditions for manipulations, including hybridization and amplification are well known in the art. The instant invention describes a method for capturing and irreversibly binding nucleic acid on a solid phase matrix immediately, and at high flow rates. Binding occurs for both DNA and RNA even at high volumes and low target concentrations. Irreversibly bound nucleic acid can be subjected to stringent aqueous washes, stored for later analysis, and repeatedly amplified or otherwise analyzed without elution and with no significant loss of bound nucleic acid. Repeated solid phase manipulation that may be accomplished according to the present invention is that of any nucleic acid.

One skilled in the art recognizes that irreversible nucleic acid binding, as disclosed herein, may be performed in a broad range of biological samples. Such samples include, for example, biological samples derived from agriculture sources, bacterial and viral sources, and from human or other animal sources, as

well as other samples such as waste or drinking water, agricultural products, processed foodstuff and air. More specifically, samples include, for example, blood, stool, sputum, mucus, cervical or vaginal specimens, cerebral spinal fluid, serum, urine, saliva, teardrop, biopsy samples, histological tissue samples, tissue culture product, an agricultural product, waste or drinking water, foodstuff and air. The present invention is useful for the irreversible binding of nucleic acid to a solid phase matrix from any sample containing nucleic acid, either naturally occurring or as a contaminant.

Various terms are used in this specification, for which it may be helpful to have definitions. These are provided herein, and should be borne in mind when these terms are used in the following examples and throughout the instant application.

As used herein, the term "archiving" refers to the analysis of nucleic acid irreversibly bound to a solid phase matrix via procedural manipulations followed by storage of the bound nucleic acid. Storage encompasses both the capacity for delayed analysis, and for repeated analysis of the same nucleic acid, as well as expanded analysis of multiple nucleic acid targets, either simultaneously or in series. For this, procedural manipulations include, for example, solid phase nucleic acid enzyme reactions, oligonucleotide or probe hybridization, and/or signal or target amplification reactions.

As used in this invention, a "template-dependent process" is defined as a process that involves either the template-dependent recognition via a specific probe, copying procedure via signal amplification reaction, or target expansion via template dependent extension of a primer molecule. A template-dependent extension refers to nucleic acid synthesis and copy expansion of RNA or DNA target sequences, wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the rules of complementary base pairing of the target nucleic acid and the primers. A template dependent process based upon complementary base pairing specifically using oligonucleotides or probes of specific sequence is known as “hybridization” detection.

A "primer" molecule refers to a nucleic acid sequence, complementary to a known portion of the target sequence/control sequence, necessary to initiate

synthesis by DNA or other polymerases.

"Target nucleic acid sequence" refers to the nucleic acid molecule that is to be detected or amplified. The target molecule can be present in a purified, partially purified or unpurified state in the sample.

"Capture" refers to the binding of nucleic acid onto a solid phase matrix. Binding can be direct in appropriate buffers based on the chemical/physical properties of nucleic acid. Alternatively, capture can be target specific by irreversibly binding probes to a solid phase matrix followed by specific hybridization.

The present invention is embodied in a method for the capture and irreversible binding of nucleic acid to a solid phase and subsequent solid phase manipulation. Regardless of the specific application of the instant invention, the methodology details are calculated according to protocols well known in the art as well as those disclosed herein. Further, the refinement of said necessary calculations is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them without undue experimentation.

This application teaches specific applications of irreversible binding of nucleic acids to solid phase materials. The known specific binding materials are characterized by atomic structure with high electropositivity that have been rendered hydrophilic. These materials have previously been considered by the skilled artisan to be of no use for nucleic acid analysis since the nucleic acid cannot be eluted. Conversely, this invention exploits this irreversible binding for specific applications.

Those skilled in the art readily recognize the present invention is broadly applicable to nucleic acid extraction, purification and detection. The following examples serve to explain and illustrate the present invention. Said examples are not to be construed as limiting of the invention in anyway. Various modifications are possible within the scope of the invention.

Example 1: Methods and Materials

DNA binding is measured utilizing ^{32}P radiolabeling. The 4361 base pair PBR322 plasmid, obtained from New England Biolabs is random prime

labeled using the Prime-It II Stratagene kit. The plasmid is cut with Hind III, unlabeled nucleotides removed utilizing BioRad Biospin 6, and adjusted to a concentration of 1 nanogram per microliter (ng/μl). Higher DNA concentrations are adjusted by the addition of salmon sperm DNA. The data for radiolabeling experiments represents the mean value of 5 replica data points.

Aluminum oxide (74-149 μm size), obtained from Aldrich (catalog no. 34,265-3), is treated with 0.1 N NaOH for 1 hour at room temperature to produce aluminum hydroxide. DNA binding buffers consisting of water (ddH_20), 0.1 N NaOH, or a 4 M guanidine thiocyanate buffer (12 g GuSCN, 277 μl Triton™ X-100, 2.2 ml 0.2 M EDTA pH 8.0, and 10 ml 0.1 M Tris-HCl pH 6.4) are used. Binding is permitted either by rotation in a closed microfuge tube or by gravity flow filtration. Large beads readily settle to the bottom of the tube without centrifugation and therefore facilitate washing. For gravity flow experiments a Spectrum SpectraMesh 43 μm filter (Spectrum, catalog no. 146530) is pressure fit into an ANSYS 4 mM chromatography column. The aluminum beads are packed into this column as a liquid slurry, allowed to drain, blotted dry, washed once with 1 ml 70% ETOH and dried prior to adding the DNA in the various binding buffers.

By way of illustration of solid phase amplification, published sequences and methods for well characterized loci are used. Further, all sequences employed in the instant experimental procedures are listed in Table I (SEQ ID NOS:1-10). Specifically, for PCR of HIV the SK38/SK39 primer set (Kellog and Kwok (1990) *In PCR Protocols: A guide to Methods and Applications*, Innis MA et al., eds., Academic Press Inc., pp. 337-347, specifically incorporated herein by reference, SEQ ID NOS. 8-9, see Table I), the control HIV DNA plasmid obtained from Perkin Elmer (catalog no. N808-0016), and rtTH reverse transcriptase amplification are used. Strand displacement amplification utilizes the mycobacterium plasmid target and primer sets described by Walker *et al.* (1996) Clinical Chemistry 42:9-13, specifically incorporated herein by reference (SEQ ID NOS:4-7, see Table I). The human Short Tandem Repeat (STR) primer sets and protocols are those commercially available from Promega, CTT and FFV multiplexes.

Example 2: Confirmation of Irreversible Solid Phase Binding of DNA.

Radiolabeled DNA (1 ng) is allowed to bind to either aluminum oxide or aluminum hydroxide at room temperature, with rotation, for 1 hour in water (ddH_20), 0.1 N NaOH, or 4 M guanidine buffer. The DNA binds to aluminum oxide in water or guanidine. Binding is greatly enhanced by using either NaOH as a binding buffer or aluminum hydroxide beads (Figure 1). In order to estimate binding capacity of 198 mg aluminum oxide, 1 ng of radiolabeled DNA is added to various concentrations of salmon sperm DNA. More specifically, this procedure estimates the point at which the aluminum becomes saturated so that binding of radiolabeled DNA is blocked (Figure 2). Water binding is saturated at 50 ng and guanidine in the range of 50 ng to 5000 ng. Sodium hydroxide binding is not saturated until 100,000 ng. Therefore, rendering aluminum hydrophilic with NaOH greatly enhances both its binding efficiency and total capacity. The irreversibility of DNA binding is shown by counting the radiolabel removed following 10 sequential washes (Figure 3). As illustrated in Figure 3, the DNA remains tightly bound with greater than 92% retention following 10 washes with 95 °C PCR buffer. The majority of eluted counts, 6%, occur during the first 4 washes with only a 2% total elution during the last 6 washes. Aluminum bound DNA is, therefore, readily amenable to aqueous washes and buffer changes without centrifugation and without danger of losing the DNA. The solid phase bound nucleic acid selected from large volume samples can be washed and then resuspended at any desired volume. For example DNA can be absorbed from a 3 milliliter (ml) sample containing guanidine, washed with phosphate or Tris buffer, then the beads resuspended in small volumes of amplification reaction mixtures (50 µl). These properties provide a method of simplifying the interface between DNA purification and amplification.

Example 3: Gravity Flow Chromatography

Significant improvement in the sensitivity of DNA detection from specimens of high volume and low concentration is derived based on

aluminum's capability of efficiently absorbing DNA at high flow rate by chromatography. Radiolabeled DNA is allowed to absorb during gravity filtration of either 74-149 μm aluminum oxide beads or 150-212 μm silica dioxide beads (Sigma, catalog no. G1145)(Figure 4). The amount of silica and aluminum is adjusted such that they both have equal surface area available for DNA binding. DNA (50 ng) binds during gravity filtration when diluted in either 1 ml (1.5-2 minutes flow time, approximately 0.5 ml/min) or 10 ml (5-8 minute flow times, approximately 2 ml/min). Aluminum is much more efficient at binding DNA during gravity flow chromatography of the 1 ml volume (SiO2 = 6% vs AlOX = 52%, both in 4 M guanidine binding buffer). Binding efficiency for both SiO2 and AlOX improves with 1 ml NaOH binding buffer (SiO2 = 12.4% vs ALOX = 60%). Increasing the flow rate four fold by using the 10 ml volume and starting with the same 50 ng DNA (i.e., 10 times lower per ml concentration than the 1 ml specimen) drastically reduces binding efficiency of silica dioxide to less than 2%. In contrast, aluminum suffers only a 10% reduction in total count recovery. Additional experimental procedures indicate that by repeating the chromatography using a second or third pass of the high volume specimen, up to 80% efficiency of binding is obtained for aluminum oxide. Aluminum is vastly superior for solid phase DNA binding compared to silica and is capable of chromatographic capture of DNA at high flow rates and low concentrations. This property allows for use of aluminum oxide for DNA concentration from pooled or large volume specimens and provides greatly increased per milliliter sensitivity of DNA detection. The high avidity of aluminum for DNA is also useful for the removal of low level DNA contaminants from water, buffers, or other reagents.

Example 4: Solid Phase Amplification

Since this nucleic acid binding is irreversible, aluminum is only useful if the bound DNA can be amplified directly on the solid phase. In order to illustrate compatibility with different amplification methods, 10^6 copies of HIV DNA and 1 μl of a plasmid prep of mycobacterium DNAs are simultaneously bound to aluminum oxide in water. These bound DNA targets are then

amplified in sequence with HIV, initially amplified using 35 cycles of polymerase chain reaction (PCR), followed by amplification of the mycobacterium target via strand displacement amplification (SDA). An ethidium bromide (EtBr) stained agarose gel of the HIV PCR, shown in Figure 5a, exhibits excellent amplification product. Following the HIV PCR amplification, the aluminum is washed four times with 70% ETOH, dried at 55 °C for 10 minutes, then an SDA amplification for the mycobacterium target is performed. An EtBr stained agarose gel of the SDA amplification also reveals amplification product at equivalent levels to those observed in the aqueous controls (Figure 5b). Additional experimental procedures show that the mycobacterium plasmid DNA is bound to aluminum using either the 4 M guanidine or 0.1 N NaOH binding buffers and SDA amplification occurs on these solid phases.

Alkaline conditions are commonly known to produce single strands. DNA is also single stranded in 4 M guanidine (Thompson and Gillespie (1987) *Analytical Biochemistry* **163**:281-291, specifically incorporated herein by reference). SDA amplification of DNA bound to aluminum oxide in NaOH or guanidine buffer proceeds without a melt step. These data confirm that in these binding buffers the DNA is bound as single strands and provides for a direct interface between DNA purification with aluminum oxide and isothermal amplification methods requiring a single stranded target nucleic acid.

To illustrate that aluminum oxide is also capable of efficient binding of RNA, the 4 M guanidine binding buffer is used to aluminum oxide purify HIV directly from an ACD plasma specimen of an AIDS patient. This specimen had previously been determined by viral load quantitative PCR to have a titer of 2 x 10^4 RNA copies per milliliter. For aluminum extraction, 0.5 ml of plasma diluted to 5 ml in 4 M guanidine thiocyanate binding buffer is used and, then gravity filtered onto 40 mg aluminum oxide. Figure 6 shows excellent PCR product formation detected on an EtBr stained agarose gel following rtTH reverse transcriptase amplification. The 4 M guanidine protocol is capable of releasing RNA from HIV virions present in plasma, and these are captured via a high volume (5 ml) gravity filtration onto aluminum oxide in an amplifiable

state. Aluminum oxide binds nucleic acids in general.

Example 5: DNA Archiving

Combining irreversibly bound nucleic acid and direct solid phase amplification, it is possible to repeatedly analyze the same DNA sample an infinite number of times. To illustrate this point, 10 µl of ACD blood is bound to aluminum in 4 M guanidine buffer. The bound DNA is then PCR amplified five times, 30 cycles each, using five sequential short tandem repeat (STR) markers from Promega. The order of amplification is: 1) F13B, 2) FESFPS, 3) VWA, 4) CTT multiplex, and 5) FFV multiplex. After the final amplification set, the DNA sample has undergone 150 PCR cycles, *in toto*. The results, shown in the silver stained gel of Figure 7, demonstrate that amplification occurs for all 5 PCRs, thus confirming DNA archiving or repeated solid phase aluminum amplification of the bound DNA.

In summary, DNA is archived onto aluminum oxide so that it is available for additional amplification analysis. This includes repeat analysis of the same gene, serial amplification of different genes, for example, to detect different infectious agents, or expanded analysis, for example, higher discriminatory power for human identity analysis.

Example 6: Buffers That Either Promote or Block Irreversible Binding of Nucleic Acid to Aluminum Oxide.

Radiolabeled DNA (50 ng) is added to 500 µl aqueous solutions of the various substances listed in Table I in the presence of 198 mg aluminum oxide. In order to more accurately measure binding exclusively of radiolabeled DNA, free unincorporated nucleotides that remain following the Biospin 6 purification are determined via TCA precipitation. As shown in Table I, using this corrected procedure, DNA binds to aluminum oxide at 100% efficiency in either 4 M guanidium or sodium hydroxide. Certain other substances and/or conditions totally block the binding of DNA. In Table I, for example, these include 10% bovine serum albumin, or K_2HPO_4. Since both binding and blocking conditions have been defined, it is therefore possible to conveniently

and specifically bind specific oligonucleotides or probes irreversibly, then change to blocking buffer conditions to allow for target specific capture by hybridization. That is, phosphate or other buffers that completely prohibit binding of nucleic acid to aluminum oxide provide the basis of hybridization buffers with low background signal to irreversibly bound nucleic acid; hybridized target is removed and the solid phase bound capture probe reused multiple times. It is well know that RNA is destroyed in 0.1 N NaOH. Therefore, by using this binding buffer DNA is exclusively captured. Efficient cell disruption and rapid nucleic acid binding with both guanidium and sodium hydroxide buffers is effective for blood, buccal swabs, urine, and HIV virions spiked into plasma or serum has. However, for certain infectious organisms, such as Cryptosporidium parvum, it is necessary to heat the specimen to 95 °C and include protein reducing agents such as dithiothreatol (DTT) in order to efficiently disrupt the cell (SEQ ID NOS:1-3, see Table II).

Example 7: Immediate Binding at High Flow Rate and Incorporation of Aluminum Oxide into PCR Tubes.

The capability of aluminum oxide to bind DNA at high flow rates is measured using the same total cpm of radiolabeled DNA suspended in 1 ml, 5 ml, or 10 ml of 4 M guanidium buffer and passing these by either aluminum oxide or silica dioxide at measured flow rates. The results, shown in Figure 8, confirm that aluminum oxide is vastly superior to silica dioxide. Aluminum oxide efficiently binds nucleic acid at flow concentration, high volume (10 ml) specimens to the 1 ml specimen with 10-fold higher per ml concentration and ten fold smaller volume. DNA binding is immediate, as illustrated by the experimental results depicted in Figure 9. Here, 50 µl of ACD anticoagulated blood is added to aluminum oxide in 0.1 N NaOH binding buffer and the HLA DR beta gene PCR amplified from the solid phase bound DNA either immediately or after permitting various incubation times for the DNA to bind. Binding as indicated by the efficiency of amplification is identical for the immediate, 1- or 2-minute time points. These experimental results are the basis of an extremely convenient and rapid protocol for automatable nucleic acid

extraction that is directly interfaced with PCR amplification. For this, aluminum oxide is adhered, via a silicon or any other adhesive shown not to inhibit PCR, into PCR tubes as shown in Figure 10. Alternatively, it may be incorporated into a 96 PCR tube plate for higher throughput. Either of these alternatives provides for simple nucleic acid extraction by a protocol consisting of the following steps: 1) adding binding buffer to the aluminum oxide PCR tube, 2) adding specimen to each tube, mixing and then aspirating liquid to waste, 3) washing by repeat pipetting wash buffer (three times), then aspirating wash buffer to waste, 4) adding PCR amplification master mix, and 5) amplifying in a thermal cycler. The pipetting steps of this protocol are easily automated for high throughput using a robotic system.

Example 8: Confirmation of Binding of Pure RNA to Aluminum Oxide

Example 4 suggested that RNA irreversibly binds and is amplifiable on aluminum oxide based upon the detection of HIV from a patient plasma specimen. It is possible that this result is due to contaminating proviral DNA in the serum. RNA binding using a pure RNA target confirms irreversible binding and solid phase amplification. Figure 11 depicts results of amplification of a pAW109 pure RNA target bound in 4 M guanidium buffer and rtPCR amplified on the aluminum oxide solid phase. Binding and amplification of IL-2 mRNA and Cryptosporidium dsRNA are demonstrated in a similar manner.

Example 9: Irreversibly Bound Nucleic Acid Utilization for Specific Target Capture by Hybridization

Limit of detection experiments determine that detection following PCR amplification of aluminum oxide bound DNA requires 1000 copies, and bound RNA requires 10^3 copies (Figure 11). Sensitivity of detection is significantly improved to less that 100 copies for either RNA or DNA using solid phase probe capture followed by hybridization. High copy capture oligonucleotide of 20-100 base pair length complementary to a sequence adjacent to the desired amplification target is irreversibly bound to aluminum oxide in 0.1 N NaOH,

buffer. After washing, this capture bead is used to hybridize to the target, even in specimens that contain high background levels of nucleic acid. For this procedure, the specimen is disrupted with 4 M guanidium buffer, diluted three fold in the presence of the solid phase matrix containing the capture probe. Hybridization is permitted to occur, and following a wash step the capture bead containing the hybridized target is directly PCR amplified. As shown in Figure 11, this results in limits of detection of from 10-100 copies of the target.

Example 10: Capture of Low Copy Targets in High Volume or Pooled Specimens.

Hybridization capture onto solid phase probe is efficient for the specific selection of target sequences even at high initial specimen volumes. As shown in Figure 12, 1000 copies of HIV from an AIDS patient plasma specimen is detectable with the hybridization solid phase capture procedures described above; detectable even when diluted to an initial volume of 5.5 mls with plasma. The plasma is added directly to dry guanidium powder for the extraction in order to minimize dilution. With this adjustment the final volume for hybridization to the capture bead is 30 mls. Additionally, positive HIV plasma at 100 µl volume is pooled with an additional 24 negative 100 µl plasma specimen, and still detected. Pooling experiments such as this confirm a detection sensitivity of 48 HIV virion copies per milliliter. Additional procedures demonstrated the detection of 100 copies of Cryptosporidium pooled in 30 mls of water. The hybridization capture bead protocol, therefore, can be used to screen pooled specimens at a sensitivity almost equivalent to that for an individual specimen, carrying tremendous commercial potential since it will allow highly sensitive pooled specimen testing and providing significant reduction of cost.

Example 11: Storage of Nucleic Acid Once Irreversibly Bound to Aluminum Oxide.

The nucleic acid from 50 µl of ACD blood is bound onto aluminum oxide using either the 4 M guanidium buffer or 0.1 N NaOH buffer. The

bound nucleic acid is then stored either dry, in 70 % EtOH, or in Tris EDTA buffer at room temperature, 4 °C, or
-20 °C. Nucleic acid is generally stable for all of these conditions for three months, and potentially much longer utilizing the instant invention -- perhaps indefinitely.

The present invention is directed to the binding of RNA to aluminum oxide and various uses for solid phase bound DNA and/or RNA. This includes methods for using aluminum oxide or other material that irreversibly binds nucleic acid for solid phase capture and directly interfaces with various manipulations; said methods using aqueous buffers, as well as for both single and in series multiplex amplification or hybridization based reactions. Further, nucleic acid capture is useful for the purpose of either removing contaminant nucleic acid, or concentrating low copy nucleic acid for the purpose of detection in either high volume or pooled specimen analysis. Aluminum oxide shows sufficient avidity for nucleic acid to bind it even at low concentrations and at high flow rates, for example, 5 ml/min. The instant invention is, thus, useful for large volume, gravity-based or high flow rate capture as well as the capture of nucleic acid in a manner compatible with extensive aqueous washes yielding extremely clean nucleic acid, free from inhibitors that may interfere with amplification reactions.

The hybridization reactions disclosed herein include direct hybridization to captured nucelci acid in the form of beads and planar surfaces, such as blots or microarray chips. Hybridization may also include the specific capture of a specific sequence by irreversibly binding capture probes, for example, oligonucleotide, cDNA, cloned plasmid, transcribed or synthesized RNA, or PNA to select the complementary sequence from a complex specimen having a high background level of non-specific nucleic acid. The capture bead methodology is useful for specific sequence capture such as by utilizing poly-T oligonucleotides bound to aluminum oxide to purify poly A messenger RNA. By using the appropriate capture oligonucleotide any specific nucleic acid target can be selectively removed and concentrated from a variety of specimen types.

Also consistent with the current invention is enzyme recognition,

specific manipulation or amplification reactions from nucleic acid irreversibly bound to a solid phase.. This includes, both target amplification reactions such as PCR, SDA, NASBA, IsoCR, or CRCA, as well as signal amplification reactions such as Q beta replicase or branched chain DNA. The incorporation of aluminum oxide as a binding substance adhered to the reaction surface area of standard PCR tubes and a protocol for rapid nucleic acid extraction that directly and conveniently interfaces with PCR thermal cycling reactions using the same tube is taught herein as well. The tubes or vessels provide a platform for automation using high throughput robotics.

Buffer systems that enable the utilization of aluminum oxide for alternative nucleic acid applications are all discussed. They include, for example, guanidium based buffer including a specific reducing agent that disrupts extremely hardy specimens, such as Cryptosporidium. In this buffer, both DNA and RNA efficiently bind to aluminum oxide at close to 100% efficiency. Another buffer system is directed to alkaline buffers such as NaOH that provide a rapid and economical DNA binding buffer. In this buffer, RNA is destroyed so that this provides a means of selectively binding only DNA. Yet, another system includes buffers that completely prohibit binding of nucleic acid to aluminum oxide, for example, phosphate buffer. This buffer system provides the basis of hybridization buffers with low background signal to noise for sensitive and efficient microarray, bead and blot hybridization.

The irreversible binding characteristics of, for example, aluminum oxide, provide for repeated analysis of either the same or different genes in series. This includes the analysis of both DNA and RNA simultaneously, or DNA and RNA independently but in series. By binding multiple probes the hybridization capture can also be multiplexed for specific targets. Thus, the instant invention is useful for repeat or in series analysis of any nucleic acid by either hybridization or amplification reactions. Once irreversibly bound, nucleic acid is stable and can be stored for prolonged periods at room temperature.

While the above description contains many specificities, these specificities should not be construed as limitations on the scope of the invention, but rather exemplification of the preferred embodiment thereof. That

is to say, the foregoing description of the invention is exemplary for purposes of illustration and explanation. Without departing from the spirit and scope of this invention, one skilled in the are can make various changes and modifications to the invention to adapt it to various usages and conditions. As such, these changes and modifications are properly, equitably, and intended to be within the full range of equivalence of the following claims. Thus, the scope of the invention should be determined by the appended claims and their legal equivalents, rather than by the examples provided herein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(I) APPLICANT: John C. Gerdes
Jeffrey M. Marmaro
Christopher A. Roehl

(ii) TITLE OF INVENTION: NUCLEIC ACID ARCHIVING

(iii) NUMBER OF SEQUENCES: 10

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch
(B) COMPUTER: IBM PC Compatible
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: WordPerfect 6.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 16 April 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/046,999
(B) FILING DATE: 16 April 1997

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(C) REFERENCE/DOCKET NUMBER: IAD-4

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(2) INFORMATION FOR SEQ ID NO:1:
(I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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21

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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20

(2) INFORMATION FOR SEQ ID NO:3:
(I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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100

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(D) TOPOLOGY: linear
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15

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(D) TOPOLOGY: linear
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(D) TOPOLOGY: linear
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(B) TYPE: nucleic acid
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(D) TOPOLOGY: linear
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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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28

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28

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40 GTCACTTCCC CTTGGTTCTC TCATCTGGCC
TGGTGCAATA 80 GGCCCTGCAT GCACTGGATG
100

TABLE I

Binding of Radiolabeled DNA to Aluminum Oxide

Binding Buffer	Percent Bound	Percent Unbound
ddH_20	20	80
0.1 N NaOH	110	0
4 M GuSCN	104	0
10% BSA	5	95
1 M K_2HPO_4	4	96
10% Triton™ X-100	64	36
10% Tween™ 20	106	0
10% SDS	12	88
5X SSC	60	40

TABLE II

ID	SEQUENCE	SEQ ID NO:
CPSR805F	GAGGATAGAGGCATTTGGTTG	SEQ ID NO:1
CPSR948R	GTTTTGTAGGGGTCGCTCAT	SEQ ID NO:2
CPSR100cap	CTATATCGTAATACGCTCTGATTACGTAGGGAGTGG TACTCCTAACAGTAGGCCTCTGATTTGTCAGTCGACA TACCGCTGCGCTCAAATCCTTTTAGAA	SEQ ID NO:3
B1	CGATCGAGCAAGCCA	SEQ ID NO:4
B2	CGAGCCGCTCGCTGA	SEQ ID NO:5
S1	ACCGCATCGAATGCATGTCTCGGGTAAGGCGTACTC GACC	SEQ ID NO:6
S2	CGATTCCGCTCCAGACTTCTCGGGTGTACTGAGATCC CCT	SEQ ID NO:7
SK38	ATAATCCACCTATCCCAGTAGGAGAAAT	SEQ ID NO:8
SK39	TTTGGTCCTTGTCTTATGTCCAGAATGC	SEQ ID NO:9
HIV cap	ATCCTATTTGTTCCTGAAGGGTACTAGTAGTTCCTGC TATGTCACTTCCCCTTGGTTCTCTCATCTGGCCTGGT GCAATAGGCCCTGCATGCACTGGATG	SEQ ID NO:10

We claim:

1. A method for archiving nucleic acid, comprising:
a) irreversibly binding single- or multiple-stranded nucleic acid contained in an aqueous specimen to a solid phase matrix;
b) manipulating said solid phase bound nucleic acid; and
c) storing said bound nucleic acid on said solid phase matrix.

2. The method as defined in claim 1 further comprising performing large volume gravity-based or high flow rate solid phase chromatography on said bound nucleic acid prior to storage.

3. The method as defined in claim 1 wherein said solidi phase matrix is selected from the group consisting of beads and planar surfaces.

4. The solid phase matrix as defined in claim 3 wherein said planar surface is selected from the group consisting of blots and microarrays.

5. The method as defined in claim 1 wherein said solid phase matrix comprises highly electropositive material rendered hydrophilic.

6. The method as defined in claim 5 wherein said highly electropositive material is selected from the group consisting of Silicon (Si), Boron (B) and Aluminum (Al).

7. The method as defined claim 1 wherein said specimen is comprised essentially of nucleic acid and buffer.

8. The specimen as defined in claim 7 wherein said buffer comprises a guanidium based buffer.

9. The specimen as defined in claim 7 wherein said buffer comprises an alkaline buffer.

10. The specimen as defined in claim 9 wherein said alkaline buffer is Sodium Hydroxide.

11. The specimen as defined in claim 7 wherein said buffer comprises a phosphate buffer.

12. The method as defined in claim 1 wherein direct manipulation methodology is selected from the group consisting of enzyme reactions, oligonucleotide hybridization, probe hybridization, signal amplification and target amplification

13. The manipulation as defined in claim 12 wherein said amplification methodology is selected from the group consisting of PCR, SDA, NASBA, IsoCR, CRCA, Q beta replicase and branched chain DNA.

14. The manipulation as defined in claim 12 wherein said hybridization methodology is selected from the group consisting of direct and specific capture hybridization.

15. The method as defined in claim 1 wherein said nucleic acid is naturally occurring.

16. The method as defined in claim 1 wherein said nucleic acid is non-naturally occurring.

17. The method as defined in claim 1 wherein said archiving is adapted for use in a standard polymerase chain reaction tube.

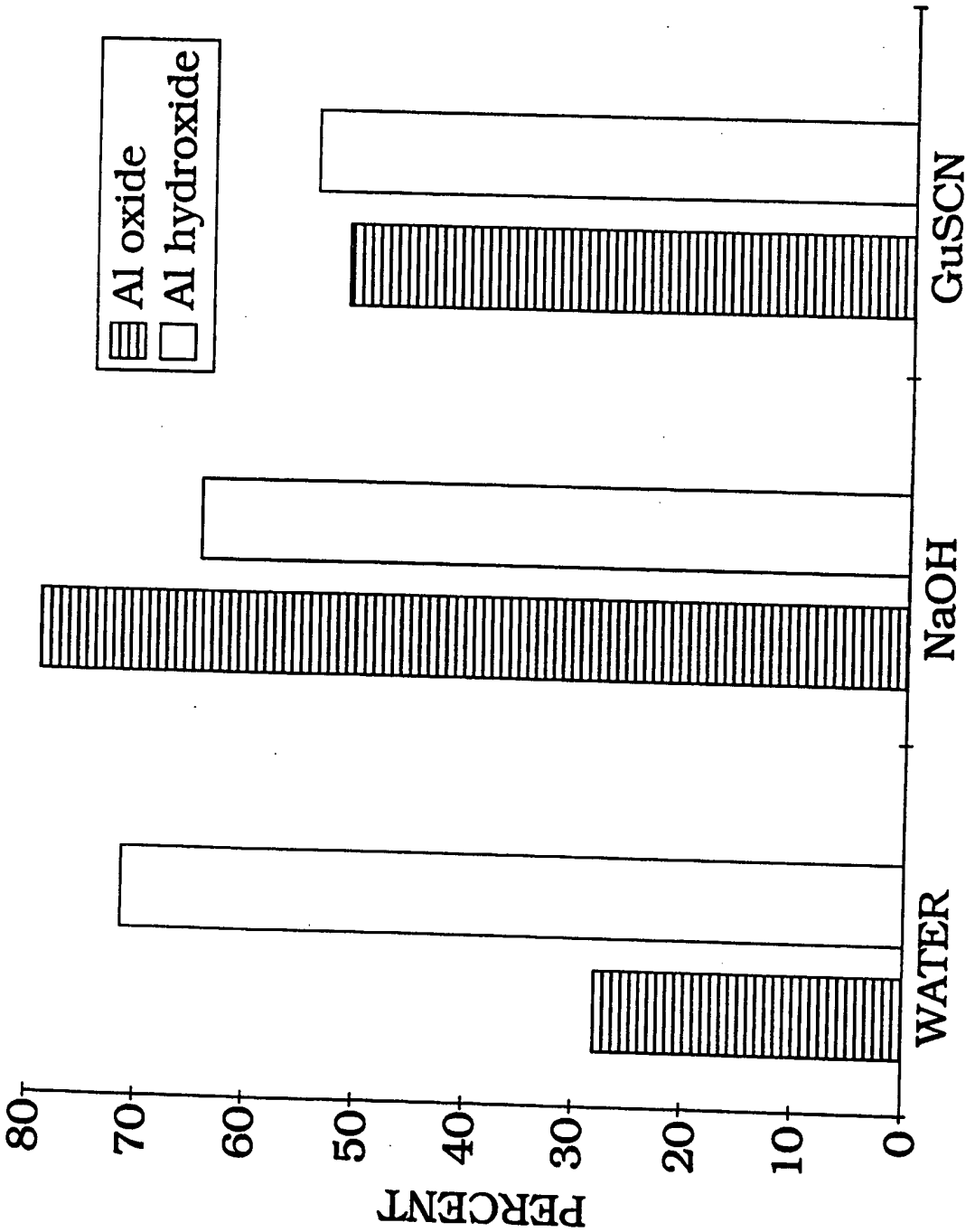
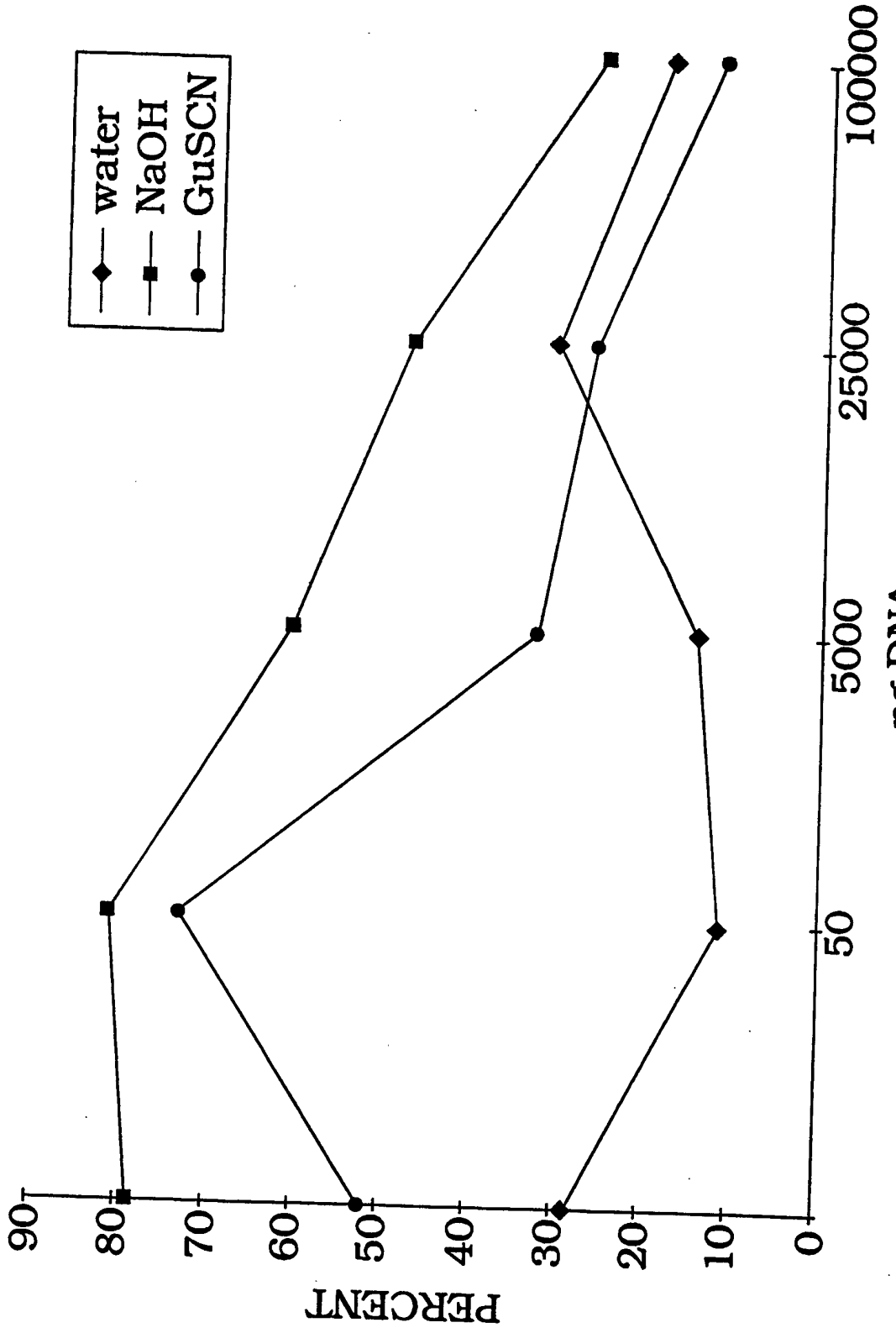

Al oxide
Al hydroxide
PERCENT
80
70
60
50
40
30
20
10
0
WATER
NaOH
GuSCN

FIG. 1


water
NaOH
GuSCN
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60
70
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50
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25000
100000
ng DNA

FIG. 2

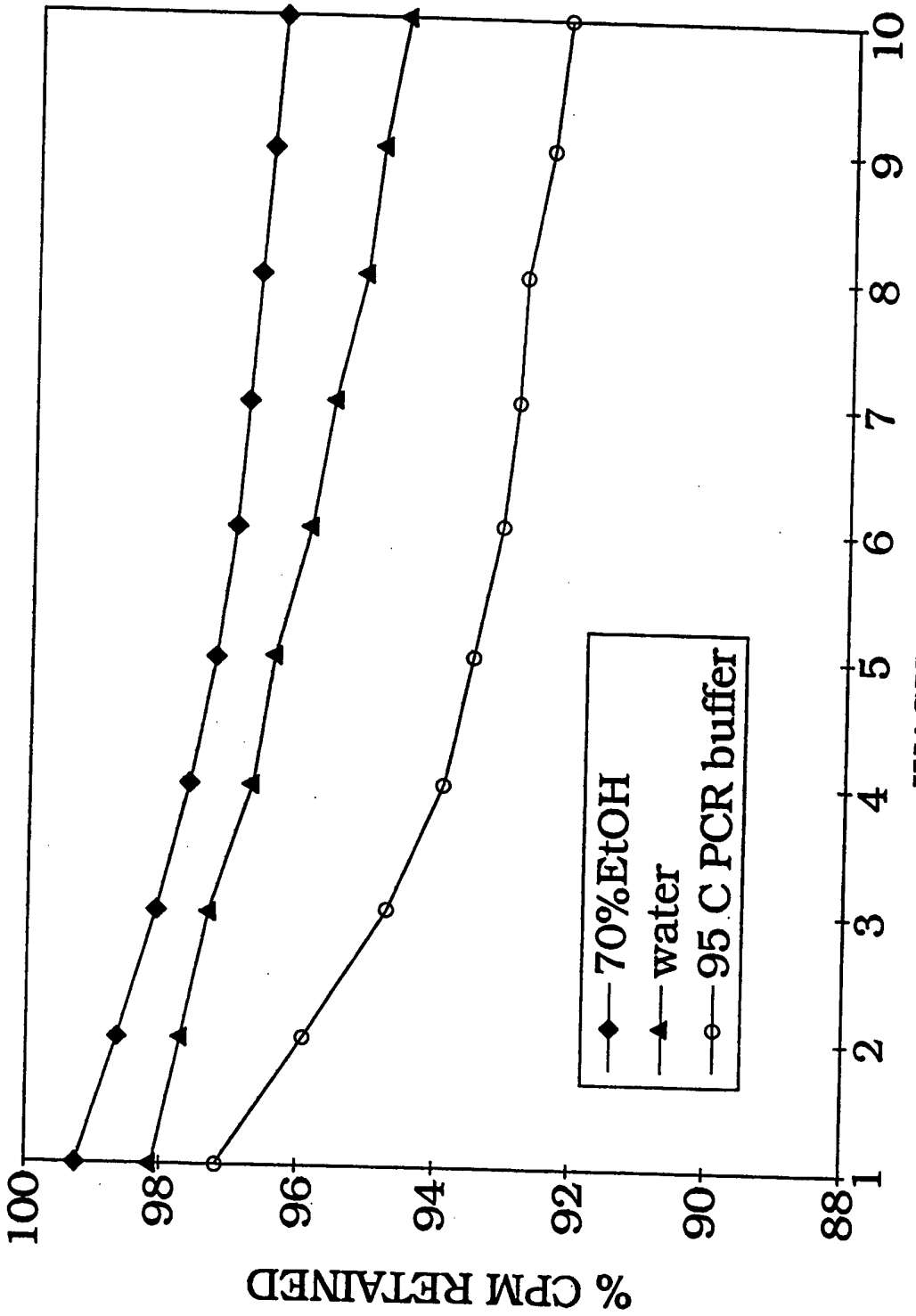

% CPM RETAINED
100
98
96
94
92
90
88
1
2
3
4
5
6
7
8
9
10
WASH NUMBER
70%EtOH
water
95 C PCR buffer

FIG. 3

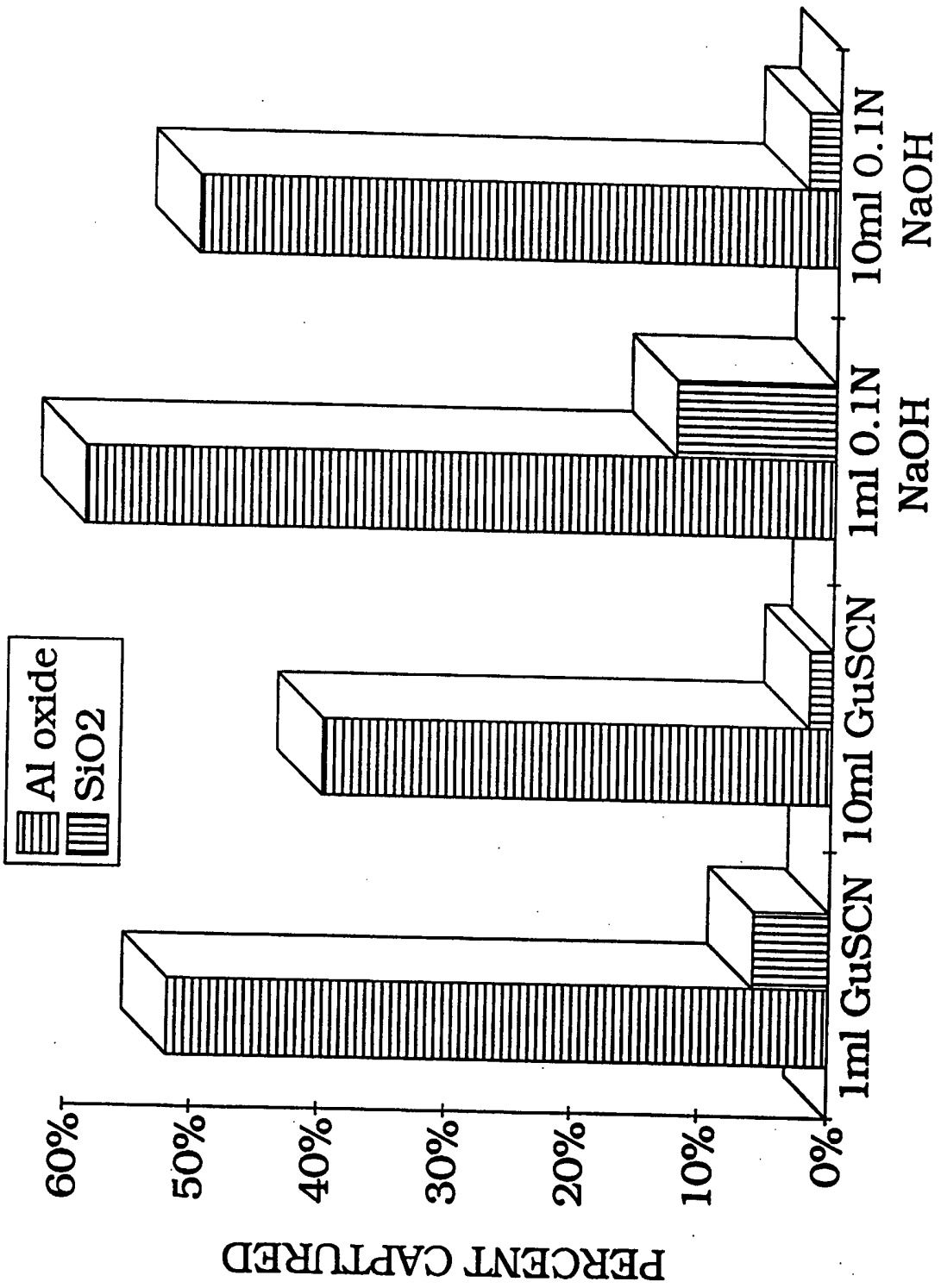

PERCENT CAPTURED
60%
50%
40%
30%
20%
10%
0%
Al oxide
SiO2
1ml GuSCN
10ml GuSCN
1ml 0.1N NaOH
10ml 0.1N NaOH

FIG. 4

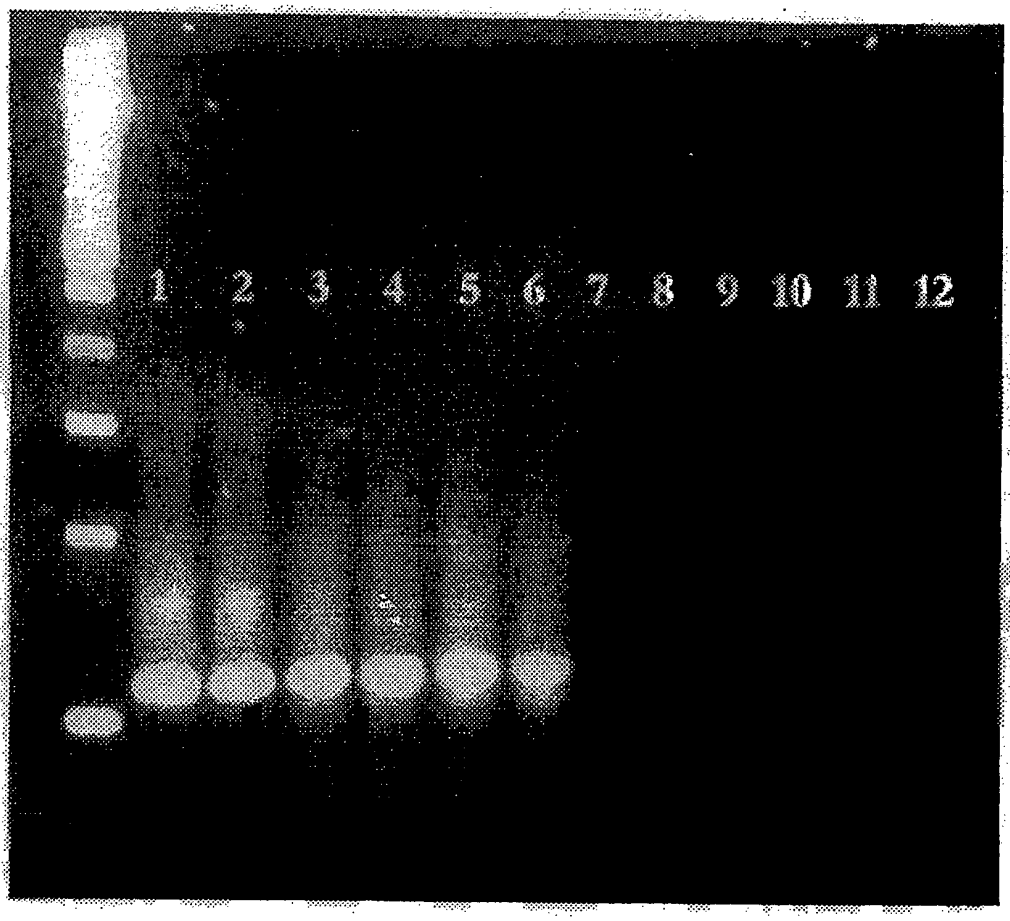


FIG. 5A

FIG.5B

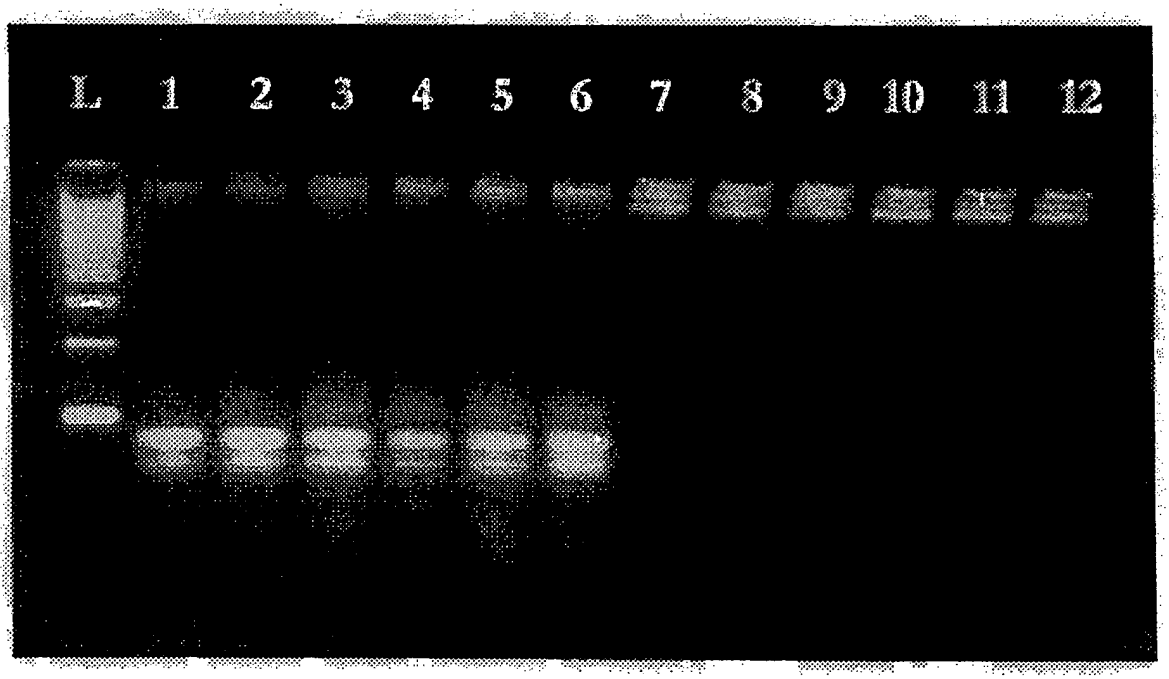


FIG. 6

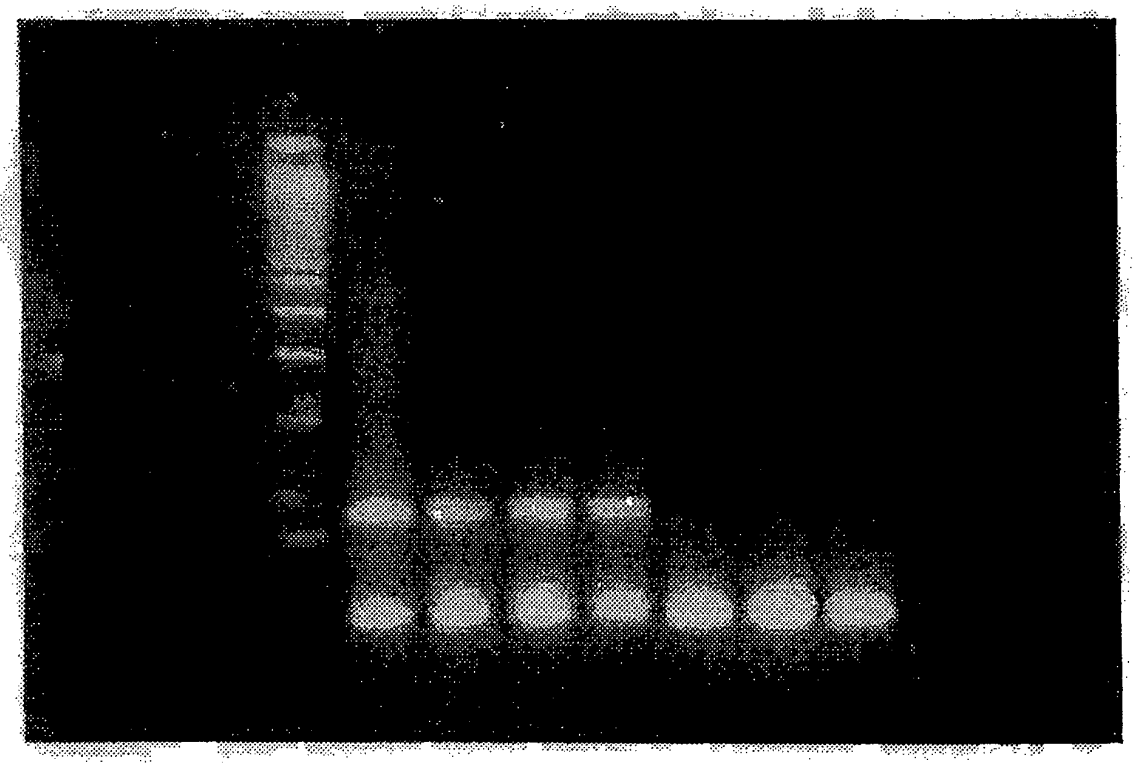
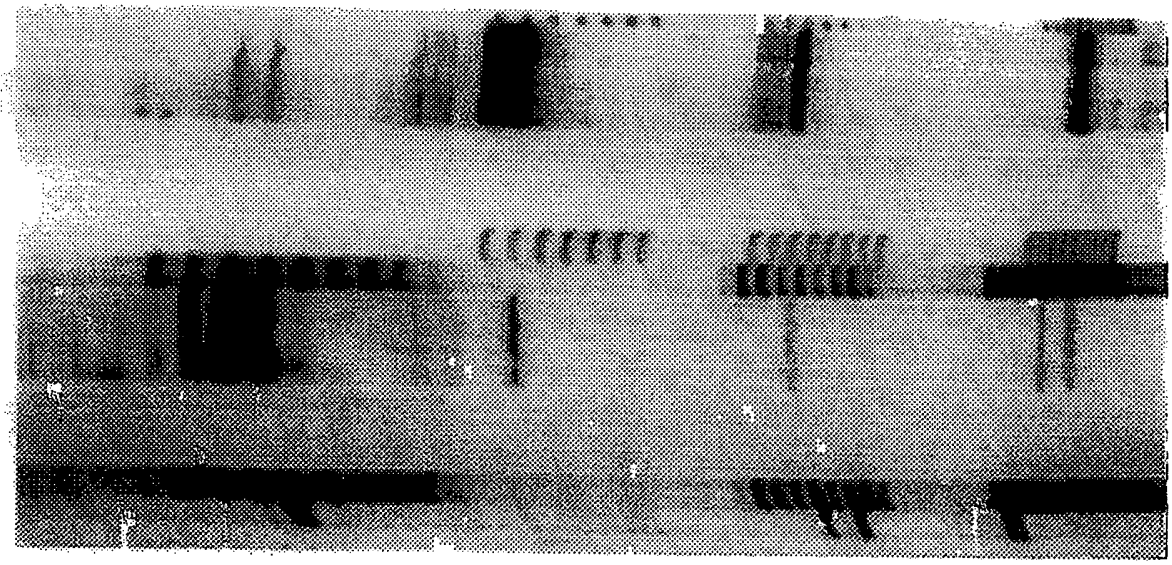


FIG. 7



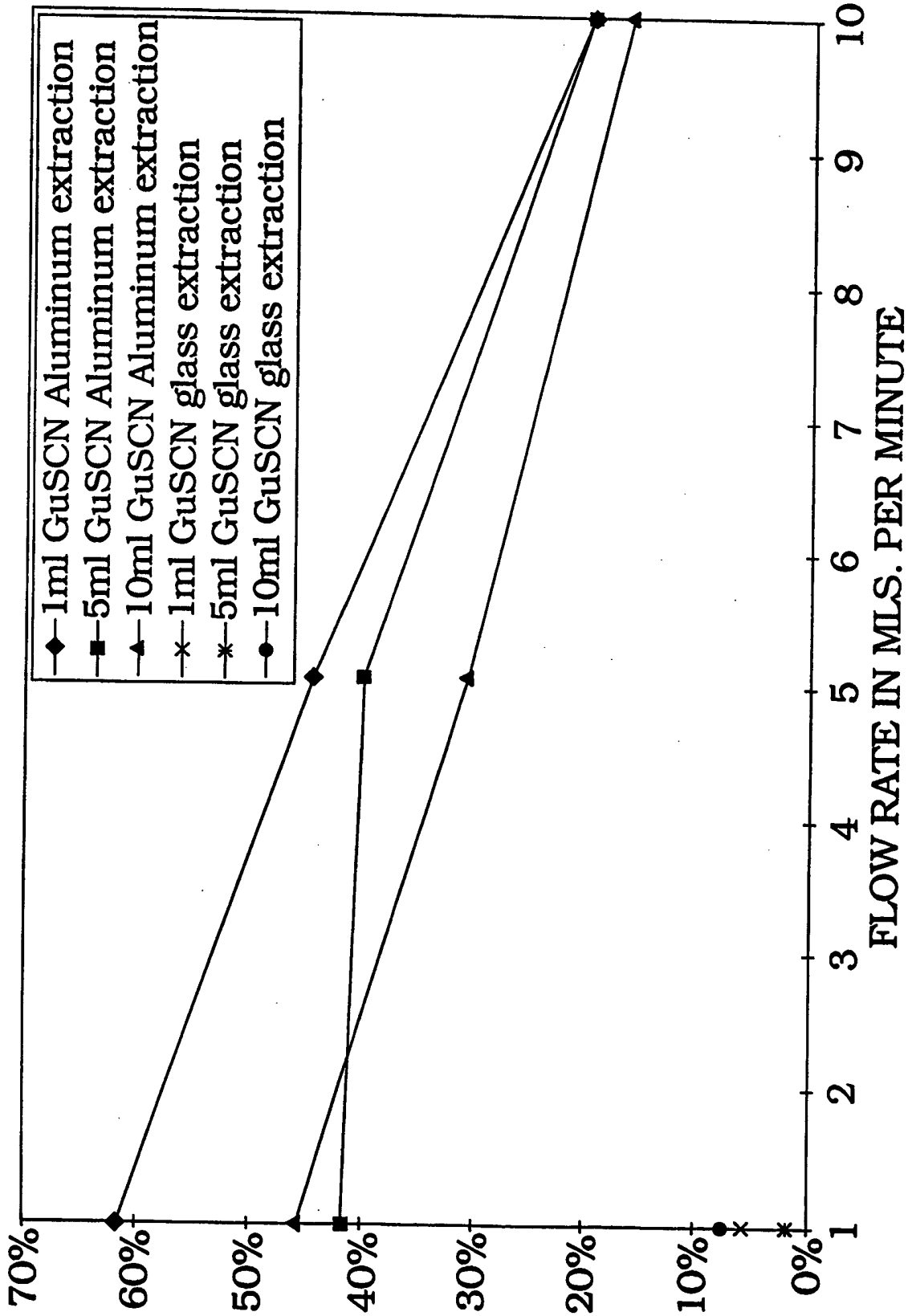

1ml GuSCN Aluminum extraction
5ml GuSCN Aluminum extraction
10ml GuSCN Aluminum extraction
1ml GuSCN glass extraction
5ml GuSCN glass extraction
10ml GuSCN glass extraction
70%
60%
50%
40%
30%
20%
10%
0%
1
2
3
4
5
6
7
8
9
10
FLOW RATE IN MLS. PER MINUTE

FIG. 8

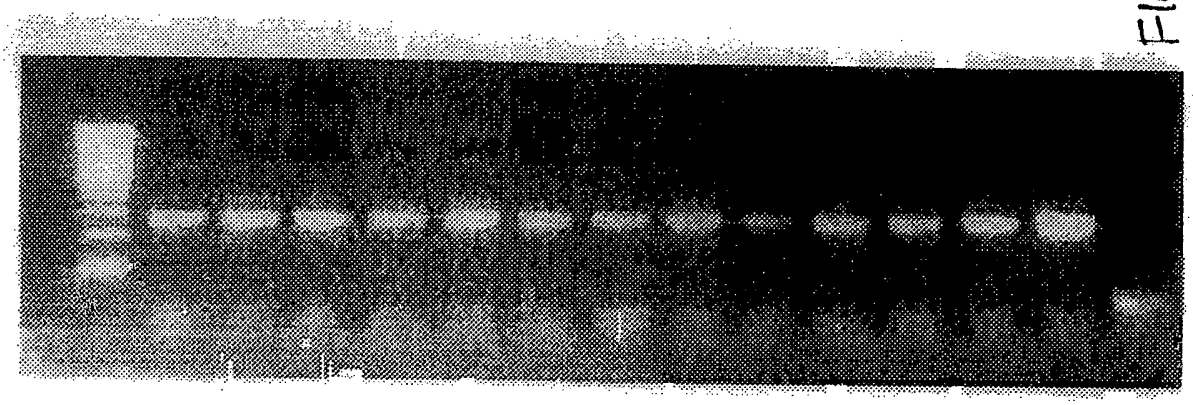
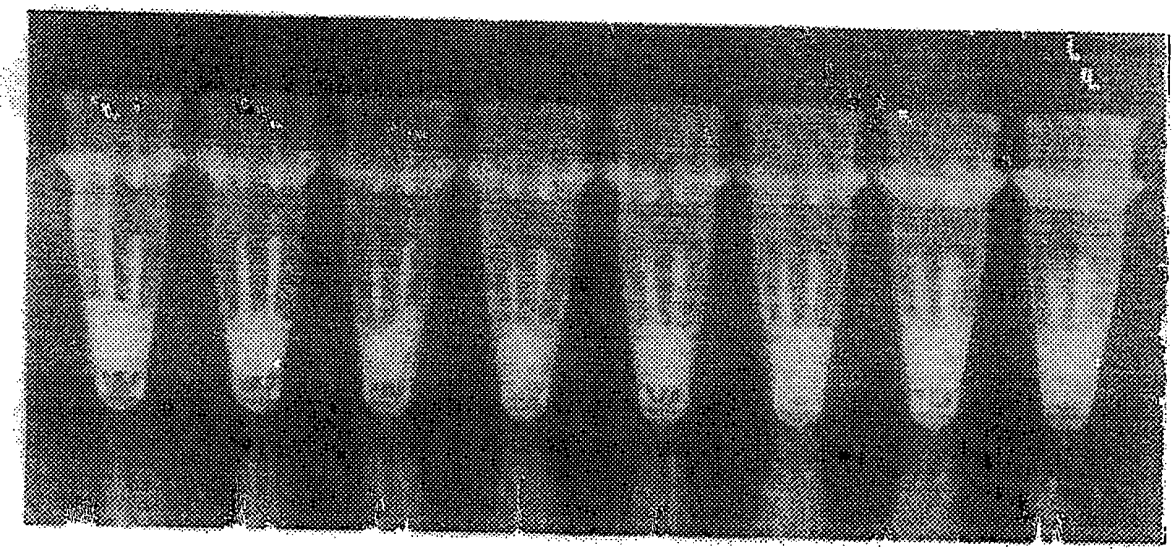
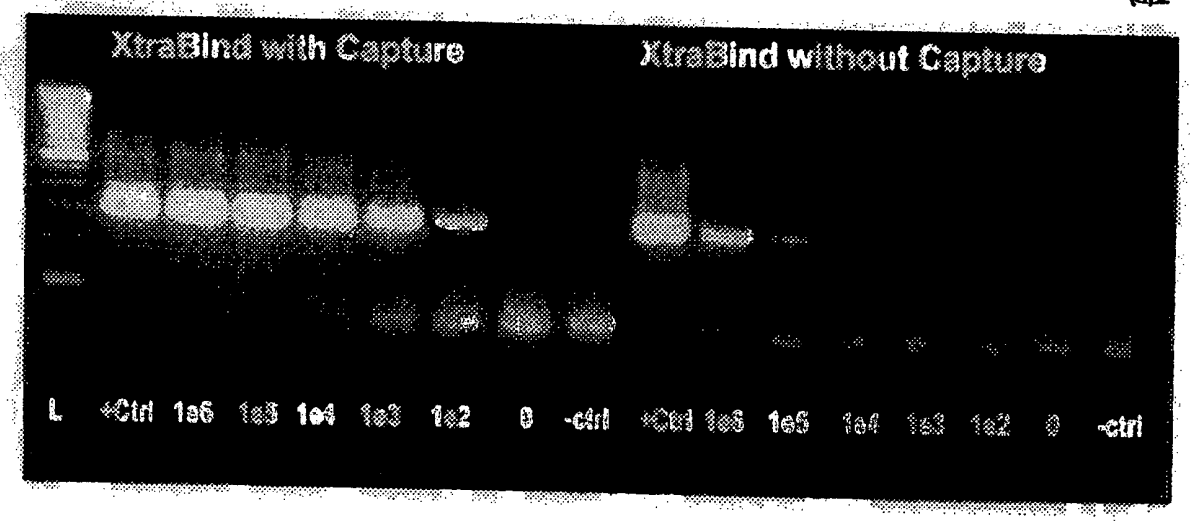


FIG. 9

FIG. 10




XtraBind with Capture
XtraBind without Capture
L
+Ctrl
1e6
1e5
1e4
1e3
1e2
0
-ctrl
+Ctrl
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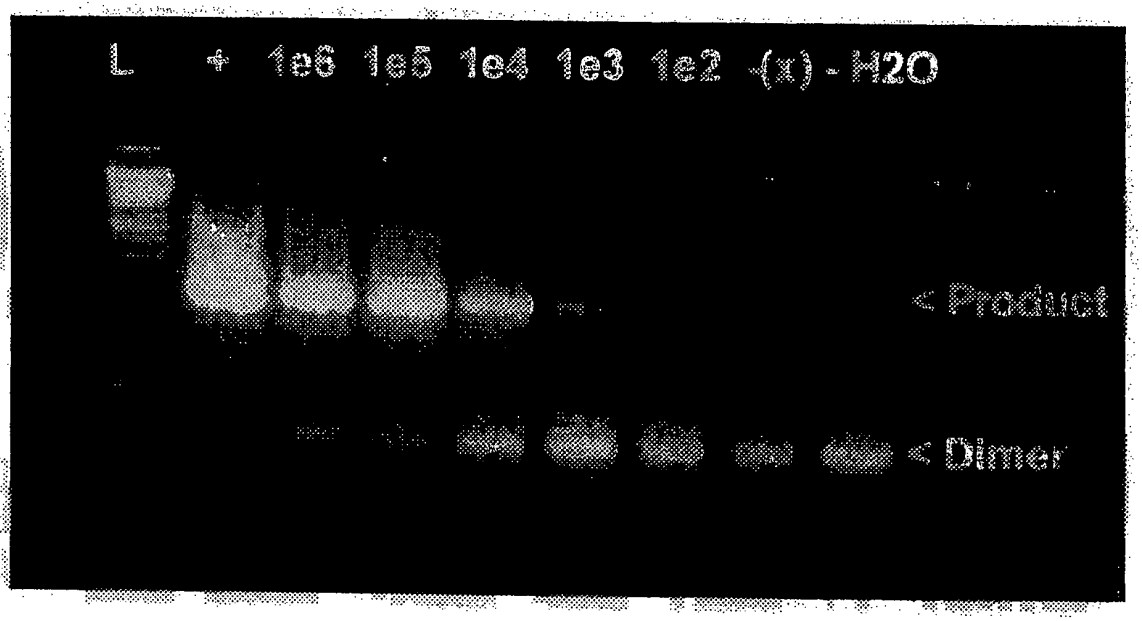
1e3
1e2
0
-ctrl

FIG. 11

FIG. 12



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/07707

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12Q 1/68; C12P 19/34
US CL : 435/6, 91.2, 91.5, 91.51
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.2, 91.5, 91.51; 536/24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Searched inventors and keywords immobilize and covalent or irreversible and nuclacid acid and storage or archiving or bank or database in APS, CAPLUS, MEDLINE, SCISEARCH, WPIDS.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,514,785 A (VAN NESS et al) 07 May 1996, col. 11-12, especially col. 12 line 40.	1-17
A	RASMUSSEN et al. Covalent Immobilization of DNA onto Polystyrene Microwells: The Molecules Are Only Bound at the 5' End. Analytical Biochemistry. October 1991, Vol. 198, No. 1, pages 138-142, see page 139.	1-17
A	SOUTHERN et al. Analyzing and Comparing Nucleic Acid Sequences by Hybridization to Arrays of Oligonucleotides: Evaluation Using Experimental Models. Genomics. August 1992, Vol. 13, pages 1008-1017, see page 1009.	1-17

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 15 JULY 1998	Date of mailing of the international search report 19 AUG 1998
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks	Authorized officer

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/07707

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	BEATTIE et al. Advances in Geosensor Research. Clinical Chemistry. May 1995, Vol. 41, No. 5, pages 700-706, see entire document.	1-17